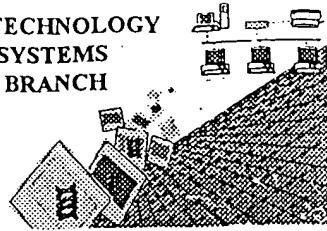


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/550,163B
Source: 1FW16
Date Processed by STIC: 12/29/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/550,1638</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules , each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/550,163B

DATE: 12/29/2003

TIME: 18:29:45

Input Set : A:\09550163b.txt

Output Set: N:\CRF4\12292003\I550163B.raw

3 <110> APPLICANT: University of Utah Research Foundation
 4 Yale University
 5 Abbott, Geoffrey W
 6 Sesti, Federico
 7 Splawski, Igor
 8 Keating, Mark T
 9 Goldstein, Steve A.N.
 11 <120> TITLE OF INVENTION: MinK-Related Genes, Formation of Potassium Channels and
 12 Association with Cardiac Arrhythmia
 14 <130> FILE REFERENCE: 2323-150.a
 16 <140> CURRENT APPLICATION NUMBER: 09/550,163B
 17 <141> CURRENT FILING DATE: 2000-04-14
 19 <150> PRIOR APPLICATION NUMBER: US 60/129,404
 20 <151> PRIOR FILING DATE: 1999-04-15
 22 <160> NUMBER OF SEQ ID NOS: 22
 23 <170> SOFTWARE: PatentIn version 3.1/2.0

Does Not Comply
 Corrected Dockette Needed
 1/3

ERRORED SEQUENCES

774 <210> SEQ ID NO: 21
 775 <211> LENGTH: 130
 776 <212> TYPE: PRT
 777 <213> ORGANISM: *rattus norvgecicus*
 E--> 779 <400> SEQUENCE: (321)
 781 Met Ala Leu Ser Asn Ser Thr Thr Val Leu Pro Phe Leu Ala Ser Leu
 782 1 5 10 15
 785 Trp Gln Glu Thr Asp Glu Pro Gly Gly Asn Met Ser Ala Asp Leu Ala
 786 20 25 30
 789 Arg Arg Ser Gln Leu Arg Asp Asp Ser Lys Leu Glu Ala Leu Tyr Ile
 790 35 40 45
 793 Leu Met Val Leu Gly Phe Phe Gly Phe Thr Leu Gly Ile Met Leu
 794 50 55 60
 797 Ser Tyr Ile Arg Ser Lys Lys Leu Glu His Ser His Asp Pro Phe Asn
 798 65 70 75 80
 801 Val Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Gly Lys Ala Leu Phe
 802 85 90 95
 805 Gln Ala Arg Val Leu Glu Ser Phe Arg Ala Cys Tyr Val Ile Glu Asn
 806 100 105 110
 809 Gln Ala Ala Val Glu Gln Pro Ala Thr His Leu Pro Glu Leu Lys Pro
 810 115 120 125
 813 Leu Ser
 814 130

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/550,163B

DATE: 12/29/2003

TIME: 18:29:45

Input Set : A:\09550163b.txt

Output Set: N:\CRF4\12292003\I550163B.raw

817 <210> SEQ ID NO: 22

818 <211> LENGTH: 129

819 <212> TYPE: PRT

820 <213> ORGANISM: homo sapiens

E--> 823 <400> SEQUENCE: 422

825	Met	Ile	Leu	Ser	Asn	Thr	Thr	Ala	Val	Thr	Pro	Phe	Leu	Thr	Lys	Leu
826	1					5				10					15	
829	Trp	Gln	Glu	Thr	Val	Gln	Gln	Gly	Gly	Asn	Met	Ser	Gly	Leu	Ala	Arg
830						20				25				30		
833	Arg	Ser	Pro	Arg	Ser	Gly	Asp	Gly	Lys	Leu	Glu	Ala	Leu	Tyr	Val	Leu
834						35			40				45			
837	Met	Val	Leu	Gly	Phe	Phe	Gly	Phe	Phe	Thr	Leu	Gly	Ile	Met	Leu	Ser
838						50			55			60				
841	Tyr	Ile	Arg	Ser	Lys	Lys	Leu	Glu	His	Ser	Asn	Asp	Pro	Phe	Asn	Val
842	65					70				75				80		
845	Tyr	Ile	Glu	Ser	Asp	Ala	Trp	Gln	Glu	Lys	Asp	Lys	Ala	Tyr	Val	Gln
846						85				90			95			
849	Ala	Arg	Val	Leu	Glu	Ser	Tyr	Arg	Ser	Cys	Tyr	Val	Val	Glu	Asn	His
850						100			105			110				
853	Leu	Ala	Ile	Glu	Gln	Pro	Asn	Thr	His	Leu	Pro	Glu	Thr	Lys	Pro	Ser
854						115			120			125				
857	Pro															

see p. 3

09/550, 163B

3

<210> 19
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HA residues for epitope mapping

<220>
<221> PEPTIDE
<222> (10)
<223> Xaa represents encoded stop codon.

<400> 19
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Xaa
1 5 10

Xaa cannot represent a stop codon,

Since a stop codon cannot encode an amino acid
(see item 13 on Error summary sheet)

Same error in sequence 20

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/550,163B

DATE: 12/29/2003

TIME: 18:29:46

Input Set : A:\09550163b.txt

Output Set: N:\CRF4\12292003\I550163B.raw

L:751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0

L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0

L:779 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:3

L:823 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:4